

241421.txt
SEQUENCE LISTING

<110> Sewalt, Vincent
Hastings, Craig
Meeley, Robert
Hantke, Sabine
Jung, Rudolf
Everard, John
Allen, Stephen

<120> COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF
PROTEINS

<130> 5718-119 (035718/241421)

<150> 60/250,703

<151> 2000-12-01

<160> 25

<170> PatentIn version 3.0

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<211> 797

<212> DNA

<213> Zea mays

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<221> CDS

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120

cgctactccg ctccccctca gtcctcagtt cctcacctag cggtagcgtg cgcgcgggag
180

acgtag atg gcg gct tcg gag gcg gca gcg gcg gcg gca aca ccg gtg
228

Met	Ala	Ala	Ser	Glu	Ala	Ala	Ala	Ala	Ala	Ala	Thr	Pro	Val
1			5						10				

acg ccg aca gag ggg acg gtg atc gcg atc cac agc ctg gag gag tgg
276

Thr	Pro	Thr	Glu	Gly	Thr	Val	Ile	Ala	Ile	His	Ser	Leu	Glu	Glu	Trp
15					20				25				30		

agc atc cag atc gag gag gcc aac agc gcc aag aag ctg gtg gtg att
324

Ser	Ile	Gln	Ile	Glu	Glu	Ala	Asn	Ser	Ala	Lys	Lys	Leu	Val	Val	Ile
				35					40				45		

gac ttc act gca aca tgg tgt cct ccg tgc cgc gcc atg gct cca att
372

Asp Phe Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile

100549 120307

1005429-120301

241421.txt

50 55 60

ttt gct gat atg gcc aag aag tcc cca aat gtt gtt ttc ctg aaa gtt
420
Phe Ala Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val
65 70 75

gat gtg gat gaa atg aag acc att gct gag caa ttc agc gta gag gcc
468
Asp Val Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala
80 85 90

atg cca aca ttc ctg ttc atg agg gag ggc gac gtc aag gac agg gtc
516
Met Pro Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val
95 100 105 110

gtt ggc gca gca aag gaa gag cta gca agg aag ctt gaa cta cac atg
564
Val Gly Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met
115 120 125

gcc tcg tag atcagtgatg ccgtaatgta gtattgcct aaataagagg
613
Ala Ser

acgcctcgcc tcaactctga gaaaactagt gcttctgtga tggtaattcg tatgagagag
673

tgcccccttt ggtggtactt cttcgtatgt agtattaact cctgtcttaa tatgttgccc
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Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp Ser Ile
20 25 30

Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile Asp Phe
35 40 45

SECRET

241421.txt

350
 Asp Val Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala
 80 85 90

atg cca aca ttc ctg ttc atg agg gag ggc gac gtc aag gac agg gtc
 398
 Met Pro Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val
 95 100 105 110

gtt ggc gca gca aag gaa gag cta gca agg aag ctt gaa cta cac atg
 446
 Val Gly Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met
 115 120 125

gcc tcg tag atcagtgatg ccgtaatgta gtattcgctt aaataagagg
 495
 Ala Ser

acgcctcgcc tcaactctga gaaaactagt gcttctgtga tggttaattcg tatgagagag
 555

tgcccccttt ggtggtactt cttcgtatgt agtattaact cctgtcttaa tatggtgccc
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tgcttgtgct tttcatacca tgtttgctct ttcagctgag gtgttatagc gtaaatcgga
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Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp Ser Ile
 20 25 30

Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile Asp Phe
 35 40 45

Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile Phe Ala
 50 55 60

241421.txt

Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val Asp Val
65 70 75 80

Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala Met Pro
85 90 95

Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val Val Gly
100 105 110

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95
Ala Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val
20 25 30

ctt gtc aag gat ggg aag gag gta agc cgt gtg gtt ggg gcc aag aag
143
Leu Val Lys Asp Gly Lys Glu Val Ser Arg Val Val Gly Ala Lys Lys
35 40 45

gac gag ctt gag agg aag atc cgg atg ttc acg tca tct tcc tca tcg
191
Asp Glu Leu Glu Arg Lys Ile Arg Met Phe Thr Ser Ser Ser Ser
50 55 60

taa actcctgtgg ttcgcctggg acggagttgc tgaagtgaag tggcccttc
244

tctcaatgct gaaaaaaggg ggaaaaacta tgtgaaaatg atggtagacg tgtctgggtc
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agtaataaga gtttctaaaa tctgaatgag atttgaatcg ctttccgttg ctgaaaaaaa
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Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val Leu
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 103

Thr Leu Val Thr Pro Pro Pro Pro Ala Ala Asp Asp Pro Asn Cys Ala
 10 15 20

gtg gtg gcc gcg cac tcc aag gcc acc tac gac gag cag tgg gcg gcc
 151

Val Val Ala Ala His Ser Lys Ala Thr Tyr Asp Glu Gln Trp Ala Ala
 25 30 35

cac aag agc agc agc aag ctg atg gtg atc gac ttc tcg gcg tcc tgg
 199

His Lys Ser Ser Ser Lys Leu Met Val Ile Asp Phe Ser Ala Ser Trp
 40 45 50

tgc ggg ccc tgc cgc ttc atc gag ccg gcc ttc aag gag ctg gcc tcc
 247

Cys Gly Pro Cys Arg Phe Ile Glu Pro Ala Phe Lys Glu Leu Ala Ser
 55 60 65 70

241421.txt

cgc ttc acc gat gcc atc ttc atc aag gtc gac gtc gac gag ctc gcg
295 .
Arg Phe Thr Asp Ala Ile Phe Ile Lys Val Asp Val Asp Glu Leu Ala
75 80 85

gag gtc gca agg aca tgg aag gta gag gcg atg cca acg ttc gtg ctg
343
Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val Leu
90 95 100

gtc aag gat ggg aag gag gta ggc cgt gtg att ggg gct aag aag gac
391
Val Lys Asp Gly Lys Glu Val Gly Arg Val Ile Gly Ala Lys Lys Asp
105 110 115

gag ctt gag agg aag atc agg atg ttc gtc acg tca tct tcc tcg tcc
439
Glu Leu Glu Arg Lys Ile Arg Met Phe Val Thr Ser Ser Ser Ser Ser
120 125 130

taa cttagcagtg catacactcc caccttatta ctggtttctc gactccagtg
492

gttcgcctgg gacgggggtg ctgaaatggt tcccttctct gaatactgaa aaatcaaaaa
552

aagaagtata tgaaaaaatg atggtagacg tgtctggggtc aataagagtt tctgaaactt
612

ggatttgtat gtgtcagtct ctgtgttctg tttccaagga atggatcatg tgagtttgga
672

atatagctgg aaatatgttg tgctgttaaa aaaaaaaaaa aaaaaaaaa
720

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Met Gly Ser Phe Phe Ser Thr Leu Val Thr Pro Pro Pro Pro Ala Ala
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Asp Asp Pro Asn Cys Ala Val Val Ala Ala His Ser Lys Ala Thr Tyr
20 25 30

Asp Glu Gln Trp Ala Ala His Lys Ser Ser Ser Lys Leu Met Val Ile
35 40 45

Asp Phe Ser Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Glu Pro Ala
50 55 60

241421.txt

Phe Lys Glu Leu Ala Ser Arg Phe Thr Asp Ala Ile Phe Ile Lys Val
65 70 75 80

Asp Val Asp Glu Leu Ala Glu Val Ala Arg Thr Trp Lys Val Glu Ala
85 90 95

Met Pro Thr Phe Val Leu Val Lys Asp Gly Lys Glu Val Gly Arg Val
100 105 110

Ile Gly Ala Lys Lys Asp Glu Leu Glu Arg Lys Ile Arg Met Phe Val
115 120 125

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113

Met Ala Ser Glu Glu Glu Gly Val Val Ile
1 5 10

gcc tgc cac acc aag gcc gac ttc gac gcc cac atg gcc aag gcc aag
161

Ala Cys His Thr Lys Ala Asp Phe Asp Ala His Met Ala Lys Ala Lys
15 20 25

gag gcc ggc aag ctg gtg atc att gac ttc acg gcc tcc tgg tgc ggc
209

Glu Ala Gly Lys Leu Val Ile Ile Asp Phe Thr Ala Ser Trp Cys Gly
30 35 40

ccc tgc cgc ttc atc gcg cca ctg ttc gtc gag cac gcc aag aag ttc
257

Pro Cys Arg Phe Ile Ala Pro Leu Phe Val Glu His Ala Lys Lys Phe
45 50 55

acc cag gct gtg ttc ctg aag gtg gac gtg gac gag ctg aag gaa gtt
305

Thr Gln Ala Val Phe Leu Lys Val Asp Val Asp Glu Leu Lys Glu Val
60 65 70

1005429 "624500T
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gcc gcg gcc tac gat gtc gag gcg atg ccg acc ttc cac ttc gtc aag
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Ala Ala Ala Tyr Asp Val Glu Ala Met Pro Thr Phe His Phe Val Lys
75 80 85 90

aac ggg gtg acg gtc gag acc gtc gtc ggt gcc agg aag gag aac ctc
401

Asn Gly Val Thr Val Glu Thr Val Val Gly Ala Arg Lys Glu Asn Leu
95 100 105

ctg gcc cag atc gag aag cac tgc gcc gcg gcc gtg cct gct gcg tct
449

Leu Ala Gln Ile Glu Lys His Cys Ala Ala Ala Val Pro Ala Ala Ser
110 115 120

gcg tag agaggatgga ccagcacgtg gcggtggcgg tggcggttgt cttgtcggtt

505

Ala

tcagtttggg cttgtcagct gtggctgggt ggttgattgt gaactggagc atgcagtttt
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actctgggag cccatcattt ggttggctca ggtgtcaata atctgtatac cttaatcatg
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gatagttggt gtgagttgtg attggacttt ggaatttgga tgtctggctt cgttctgtta
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tgatgatgat gatggattga aaaaaaaaaa aaaaaaa

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<210> 10

<211> 123

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<213> Zea mays

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Met Ala Ser Glu Glu Glu Gly Val Val Ile Ala Cys His Thr Lys Ala
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20 25 30

Ile Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala
35 40 45

Pro Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Ala Val Phe Leu
50 55 60

Lys Val Asp Val Asp Glu Leu Lys Glu Val Ala Ala Ala Tyr Asp Val
65 70 75 80

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Page 10

1005429.102021

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                                105
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gcc cag atc gag aag cat gcc gcg cct gcg cct gcg tct gcg tct gcc
449
Ala Gln Ile Glu Lys His Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala
110 115 120

taa aggagatcag atcagtcgtc gccgtcaata agggccagca cgtatggctg
502

taaatgttgt cgttatcagt tctggctttg tcgtttgtgg gcgattgtga actagtagta
562

tgtttgtttc tatccgagcc ggaggcgata cttaaccatg gatacttggt gtgagttcgt
622

ttctgttcgc gtgtgactct tgaattgaat caaccagctc accactgcac caggccgtgg
682

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727

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<213> Zea mays

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Phe Asp Ala His Met Thr Lys Ala Gln Glu Ala Gly Lys Leu Val Val
20 25 30

Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Ala Ile Ala Pro
35 40 45

Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Val Val Phe Leu Lys
50 55 60

Val Asp Val Asp Glu Val Lys Glu Val Thr Ala Ala Tyr Glu Val Glu
65 70 75 80

Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Lys Thr Val Ala Thr
85 90 95

Ile Val Gly Ala Lys Lys Asp Glu Leu Leu Ala Gln Ile Glu Lys His
100 105 110

Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala
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120

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Met Ala Ala Glu Glu
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103
Gly Ala Val Ile Ala Cys His Thr Lys Asp Glu Phe Asp Ala Arg Met
10 15 20

gcc aag gcc aag gag cag ggc aag ctg gtg gtc atc gac ttc atg gcc
151
Ala Lys Ala Lys Glu Gln Gly Lys Leu Val Val Ile Asp Phe Met Ala
25 30 35

ccc tgg tgc agt ggg tgc cag atg atg gcc ccg gtg tac gcg gac tgc
199
Pro Trp Cys Ser Gly Cys Gln Met Met Ala Pro Val Tyr Ala Asp Cys
40 45 50

gcc agc aag tac cct tcc gcg gtc ttc ctc gag gtc gac gtc gac gaa
247
Ala Ser Lys Tyr Pro Ser Ala Val Phe Leu Glu Val Asp Val Asp Glu
55 60 65

ctg ctg gaa gtc gcg aag atc tac ggc gtc cat gtg atg ccg acc ttc
295
Leu Leu Glu Val Ala Lys Ile Tyr Gly Val His Val Met Pro Thr Phe
70 75 80 85

tgc ttc atc agg aac ggc gag acg ctc gag agc ttt gct acc gtc gac
343
Cys Phe Ile Arg Asn Gly Glu Thr Leu Glu Ser Phe Ala Thr Val Asp
90 95 100

gag gac gag ctc cgg gac gcc gtc agg aag tac gcc gcc gct ggc act
391
Glu Asp Glu Leu Arg Asp Ala Val Arg Lys Tyr Ala Ala Ala Gly Thr
105 110 115

acg acg gct cct gcc tcg gcg tcc gcc taa ttcaggagat gtgatgtgta
441
Thr Thr Ala Pro Ala Ser Ala Ser Ala
120 125

gcaaatagcg cgcgcgccacc agtcgtcaat aaataaataa ataaataaat aaataaataa

501

ataaataaat aaaggccaac gtacgacgac aaattagtgg cgcgcgcggt agtagctagc
561

agagtatgcg ccgcactgt gtcgatctgc agtttggtcg tttaaaagtg attgtagtgt
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681

aaaaaaaaaa aaaaaaaaaa
700

<210> 14
<211> 126
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<400> 14

Met Ala Ala Glu Glu Gly Ala Val Ile Ala Cys His Thr Lys Asp Glu
1 5 10 15

Phe Asp Ala Arg Met Ala Lys Ala Lys Glu Gln Gly Lys Leu Val Val
20 25 30

Ile Asp Phe Met Ala Pro Trp Cys Ser Gly Cys Gln Met Met Ala Pro
35 40 45

Val Tyr Ala Asp Cys Ala Ser Lys Tyr Pro Ser Ala Val Phe Leu Glu
50 55 60

Val Asp Val Asp Glu Leu Leu Glu Val Ala Lys Ile Tyr Gly Val His
65 70 75 80

Val Met Pro Thr Phe Cys Phe Ile Arg Asn Gly Glu Thr Leu Glu Ser
85 90 95

Phe Ala Thr Val Asp Glu Asp Glu Leu Arg Asp Ala Val Arg Lys Tyr
100 105 110

Ala Ala Ala Gly Thr Thr Thr Ala Pro Ala Ser Ala Ser Ala
115 120 125

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tattggcgtg atcttacgta aaaaaaaaaa aaaaaaaaaa 241421.txt
658

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Met Ala Ala Ser Ala Thr Ala Ala Ala Val Ala Ala Glu Val Ile Ser
1 5 10 15

Val His Ser Leu Glu Gln Trp Thr Met Gln Ile Glu Glu Ala Asn Thr
20 25 30

Ala Lys Lys Leu Val Val Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro
35 40 45

Cys Arg Ile Met Ala Pro Val Phe Ala Asp Leu Ala Lys Lys Phe Pro
50 55 60

Asn Ala Val Phe Leu Lys Val Asp Val Asp Glu Leu Lys Pro Ile Ala
65 70 75 80

Glu Gln Phe Ser Val Glu Ala Met Pro Thr Phe Leu Phe Met Lys Glu
85 90 95

Gly Asp Val Lys Asp Arg Val Val Gly Ala Ile Lys Glu Glu Leu Thr
100 105 110

Ala Lys Val Gly Leu His Ala Ala Ala Gln
115 120

<210>	17
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<212>	DNA
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<221> misc_feature
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      486, 493, 501, 507, 515, 519, 532, 542, and 579 can be an a, c,
      g, or t
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tcggatccca caccgaggaa aaggagaaga gagcgagggt cggaataatg gcggccgagg
60
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241421.txt

agggtgccgt gatcgcgctgc cacaccaagg acgagttcga cgcccgcatg gccaangnon
120

aggancnggc aagctggtgg tcatcgactt catggccccc tggcgagtg ggtgccagat
180

gatggccccc gtgtacgagg actgcgccag caagtaccct tccgcggtct tcctcgaggt
240

cgacgtggac gaactgctgg aagtcgcgaa gatctacggc gtccatgtga tgccgacctt
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ctgcttcacg aggaacngcg agacgctcga nagctttgct accgtcgacg aagacgagct
360

ccgggacgcc gtcaggaagt acgcccgcgc tggcactacg acgctcctgc ctccggcgcc
420

gcctaattca gganatgtga tgtgtagcaa atagcgcgcg cgaccatcg tcnataaata
480

antaantaat aantaattaa ntaantnaag ggccncgtnc aacaacaatt tntggccccc
540

cngtattact acaaatttgc cccccctgtt tcactcgcnt
580

<210> 18
<211> 590
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (60)..(425)

<220>
<221> misc_feature
<223> "n" at position 9, 493, 537, 548, 581, and 584 can be an a, c,
g,
or t

<400> 18
gttgcaatna caacgaacag aagctctcga tctcaccgac accgaggaag aagagatca
59

atg gcg tcc gag cag gga gtc gtg atc gcg tgc cac agc aag gct gag
107
Met Ala Ser Glu Gln Gly Val Val Ile Ala Cys His Ser Lys Ala Glu
1 5 10 15

ttc gac gcc cac atg acc aag gcc cag gaa gcc ggc aag ctg gtg gtc
155
Phe Asp Ala His Met Thr Lys Ala Gln Glu Ala Gly Lys Leu Val Val
20 25 30

10005429.120301

1005429-120304
T0202T-624500T

241421.txt

atc gac ttc act gcc gcc tgg tgc ggt cca tgc cgc gcc atc gcc cca
203

Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Ala Ile Ala Pro
35 40 45

ctg ttc gtc gaa cac gcc aag aag ttc act cag gtc gtc ttc ctg aag
251

Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Val Val Phe Leu Lys
50 55 60

gtg gac gtg gac gaa gtg aag gaa gtc acc gcg gcc tac gag gtc gag
299

Val Asp Val Asp Glu Val Lys Glu Val Thr Ala Ala Tyr Glu Val Glu
65 70 75 80

gcg atg ccg acc ttc cac ttc gtc aag aac ggc aag acg gtc gcg acc
347

Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Lys Thr Val Ala Thr
85 90 95

atc gtg ggt gcc agg aag gac gag ctc ctg gcc cag atc gag aag cat
395

Ile Val Gly Ala Arg Lys Asp Glu Leu Leu Ala Gln Ile Glu Lys His
100 105 110

gcc gcg cct gcg cct gcg tct gcg tct gcc taaaggagat cagtcgtcgc
445

Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala
115 120

cgtcaataag ggccagcacg tatggctgta aatgttgctg ttatcagntc tggctttgtc
505

gtttgtgggc gattgtgaac tagtagtatg tnggttctat ccnaagccgg aggcgatctt
565

aacctgggat acttgntgng aaaaa
590

<210> 19

<211> 122

<212> PRT

<213> Zea mays

<220>

<221> misc_feature

<223> "n" at position 9, 493, 537, 548, 581, and 584 can be an a, c,
g,

or t

<400> 19

Met Ala Ser Glu Gln Gly Val Val Ile Ala Cys His Ser Lys Ala Glu
1 5 10 15

Phe Asp Ala His Met Thr Lys Ala Gln Glu Ala Gly Lys Leu Val Val
20 25 30

241421.txt

Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Ala Ile Ala Pro
35 40 45

Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Val Val Phe Leu Lys
50 55 60

Val Asp Val Asp Glu Val Lys Glu Val Thr Ala Ala Tyr Glu Val Glu
65 70 75 80

Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Lys Thr Val Ala Thr
85 90 95

Ile Val Gly Ala Arg Lys Asp Glu Leu Leu Ala Gln Ile Glu Lys His
100 105 110

Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala
115 120

<210> 20
<211> 948
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (3)..(737)

<400> 20
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47
Lys Ile Leu Thr Glu Thr Val Thr Thr Val Asp Phe Ser Ala Arg
1 5 10 15

ccc ttc cgt gtc gcc tcc gac gac acc gtt gtg cac gcc gac tcc gtc
95
Pro Phe Arg Val Ala Ser Asp Asp Thr Val Val His Ala Asp Ser Val
20 25 30

gtc gtc gcc acg ggc gcc gtc gcg cgc agg ctg cac ttc gcc ggc tcc
143
Val Val Ala Thr Gly Ala Val Ala Arg Arg Leu His Phe Ala Gly Ser
35 40 45

gac gcc ttc tgg aac cgg ggc atc tcc gcc tgc gcc gtc tgc gac ggg
191
Asp Ala Phe Trp Asn Arg Gly Ile Ser Ala Cys Ala Val Cys Asp Gly
50 55 60

gct gcg cct atc ttc cgg aac aag ccc atc gcc gtc gtc gga ggc ggg
239
Ala Ala Pro Ile Phe Arg Asn Lys Pro Ile Ala Val Val Gly Gly Gly

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65

70

75

gac tcc gcc atg gag gag gct aac ttc ctc acc aag tac ggc tcg caa
 287
 Asp Ser Ala Met Glu Glu Ala Asn Phe Leu Thr Lys Tyr Gly Ser Gln
 80 85 90 95

 gtt tac atc atc cac cgc cgc agc gac ttc cgg gcg tcc aag atc atg
 335
 Val Tyr Ile Ile His Arg Arg Ser Asp Phe Arg Ala Ser Lys Ile Met
 100 105 110

 cag gcg cgc acg ctc tcc aac ccc aag atc aag gtc gtc tgg aac tcc
 383
 Gln Ala Arg Thr Leu Ser Asn Pro Lys Ile Lys Val Val Trp Asn Ser
 115 120 125

 gag gtc gtc gag gcc tac ggc ggt gcg gat ggc ggc ccg cta gcc ggc
 431
 Glu Val Val Glu Ala Tyr Gly Gly Ala Asp Gly Gly Pro Leu Ala Gly
 130 135 140

 gtc aag gtc aag gac gtc gtc acc ggc gag gtc tct gat ctc cag gtg
 479
 Val Lys Val Lys Asp Val Val Thr Gly Glu Val Ser Asp Leu Gln Val
 145 150 155

 gcc ggg ctc ttc ttt gcc atc ggt cac gag ccg gcg aca aaa ttt ctt
 527
 Ala Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu
 160 165 170 175

 gga ggg cag ctc gag ctc gac tct gat ggg tat gtg gtg acc aag ccc
 575
 Gly Gly Gln Leu Glu Leu Asp Ser Asp Gly Tyr Val Val Thr Lys Pro
 180 185 190

 ggt tcc acg cac acc agt gtg cag ggg gtc ttt gca gct ggg gat gtc
 623
 Gly Ser Thr His Thr Ser Val Gln Gly Val Phe Ala Ala Gly Asp Val
 195 200 205

 cag gac aag aag tac cgc cag gcc att act gca gct gga tca ggt tgc
 671
 Gln Asp Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys
 210 215 220

 atg gct gct ctg gat gca gag cac tac ctg cag gag gtt gga gca cag
 719
 Met Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Val Gly Ala Gln
 225 230 235

 gaa ggg aag acc gat tga ctatgtctgg gccaaagctgc tcttgggcca
 767
 Glu Gly Lys Thr Asp
 240

 aggaaaactt ctccgaaagc cgctctctag tgggtgtaaag agcacattat tatttggttt
 827

10005429 120304

[illegible]

a
948

<400> 21

Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly

Gly Gln Leu Glu Leu Asp Ser Asp Gly Tyr Val Val Thr Lys Pro Gly
180 185 190

Ser Thr His Thr Ser Val Gln Gly Val Phe Ala Ala Gly Asp Val Gln
195 200 205

Asp Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met
210 215 220

Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Val Gly Ala Gln Glu
225 230 235 240

Gly Lys Thr Asp

<210> 22
<211> 556
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)..(336)

<400> 22
ggc ggt gcg gat ggc ggc ccg cta gcc ggc gtc aag gtc aag gac gtc
48
Gly Gly Ala Asp Gly Gly Pro Leu Ala Gly Val Lys Val Lys Asp Val
1 5 10 15
gtc acc ggc gag gtc tct gat ctc cag gtg gcc ggg ctc ttc ttt gcc
96
Val Thr Gly Glu Val Ser Asp Leu Gln Val Ala Gly Leu Phe Phe Ala
20 25 30
atc ggt cac gag ccg gcg aca aaa ttt ctt gga ggg cag ctc gag ctc
144
Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly Gly Gln Leu Glu Leu
35 40 45
gac tct gat ggg tat gtg gtg ccc aag ccc ggt tcc acg cac acc agt
192
Asp Ser Asp Gly Tyr Val Val Pro Lys Pro Gly Ser Thr His Thr Ser
50 55 60
gtg cag ggg gtc ttt gca gct ggg gat gtc cag gac aag aag tac cgc
240
Val Gln Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg
65 70 75 80
cag gcc att act gca gct gga tca ggt tgc atg gct gct ctg gat gca

241421.txt

288

Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met Ala Ala Leu Asp Ala
85 90 95

gag cac tac ctg cag gag gtt gga gca cag gaa ggg aag acc gat tga
336

Glu His Tyr Leu Gln Glu Val Gly Ala Gln Glu Gly Lys Thr Asp
100 105 110

ctatgtctgg gccaaagctgc tcttgggccca aggaaaactt ctccgaaagc cgctctctag
396

tggtgtaaac agcacattat tatttggttt taggcctcaa attacgttac attggaaatt
456

gatttatatg agcgtgcgca agcttggtata cattattcgc attgtttatt actcttagag
516

tcttagtcat taatcacact ttgctaaaaa aaaaaaaaaa
556

<210> 23
<211> 111
<212> PRT
<213> Zea mays

<400> 23

Gly Gly Ala Asp Gly Gly Pro Leu Ala Gly Val Lys Val Lys Asp Val
1 5 10 15

Val Thr Gly Glu Val Ser Asp Leu Gln Val Ala Gly Leu Phe Phe Ala
20 25 30

Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly Gly Gln Leu Glu Leu
35 40 45

Asp Ser Asp Gly Tyr Val Val Pro Lys Pro Gly Ser Thr His Thr Ser
50 55 60

Val Gln Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg
65 70 75 80

Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met Ala Ala Leu Asp Ala
85 90 95

Glu His Tyr Leu Gln Glu Val Gly Ala Gln Glu Gly Lys Thr Asp
100 105 110

<210> 24
<211> 1336

1005429.1001

<212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (91)..(1086)

<400> 24
 gaactgtaat ttcagatttc agagcgcgca agaaccctct tgaccaccgc cgccgccgcc
 60

gcgaagccaa gccaaactga gtaagcagct atg gag gga tcc gcc gcc gct ccg
 114

Met Glu Gly Ser Ala Ala Ala Pro
 1 5

ctc cgc acg cgc atc tgc atc atc ggg agc ggt ccc gct gcg cac acg
 162

Leu Arg Thr Arg Ile Cys Ile Ile Gly Ser Gly Pro Ala Ala His Thr
 10 15 20

gca gcc atc tac gcg gcc cgc gcg gag ctc aag cct gtg ctc ttc gag
 210

Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys Pro Val Leu Phe Glu
 25 30 35 40

ggc tgg atg gcc aac gac atc gcc gcg ggc ggg cag ctc acc acc acc
 258

Gly Trp Met Ala Asn Asp Ile Ala Ala Gly Gly Gln Leu Thr Thr Thr
 45 50 55

acc gac gtc gag aac ttc ccg ggc ttc ccc aac ggc atc atg ggc gcc
 306

Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Asn Gly Ile Met Gly Ala
 60 65 70

gac ctc atg gac aac tgc cgc gcg cag tcc ctg cgc ttt ggc acc aac
 354

Asp Leu Met Asp Asn Cys Arg Ala Gln Ser Leu Arg Phe Gly Thr Asn
 75 80 85

atc ctc tcc gag acc gtc acc gcc gtc gac ttt tcg gcc tgc cca ttc
 402

Ile Leu Ser Glu Thr Val Thr Ala Val Asp Phe Ser Ala Cys Pro Phe
 90 95 100

cga gtt agt gca gac tcc aca acc gtc ctc gcc gat gcg gtt atc gtt
 450

Arg Val Ser Ala Asp Ser Thr Thr Val Leu Ala Asp Ala Val Ile Val
 105 110 115 120

gcc acg gga gcc gtc gcg cgg cgc ctc cac ttc ccc ggg tcc gat gca
 498

Ala Thr Gly Ala Val Ala Arg Arg Leu His Phe Pro Gly Ser Asp Ala
 125 130 135

tac tgg aac cgc ggc atc tcc gcc tgt gcc gtc tgt gac ggt gcc gcc
 546

Tyr Trp Asn Arg Gly Ile Ser Ala Cys Ala Val Cys Asp Gly Ala Ala

1005429 100301

241421.txt

140	145	150
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ccc atc ttc cgt aac aag ccc atc gcc gtc ata ggc ggc ggc gac tcc
594
Pro Ile Phe Arg Asn Lys Pro Ile Ala Val Ile Gly Gly Gly Asp Ser
    155                      160                      165

gct atg gag gag tcc aat ttc ctc acc aag tac ggc tcc cac gtc tac
642
Ala Met Glu Glu Ser Asn Phe Leu Thr Lys Tyr Gly Ser His Val Tyr
    170                      175                      180

atc atc cac cgc cgc aat acc ttc cgt gct tcc aag atc atg cag gcc
690
Ile Ile His Arg Arg Asn Thr Phe Arg Ala Ser Lys Ile Met Gln Ala
185                      190                      195                      200

agg gcg ctt gag aac ccc aaa att aag gtc ctc tgg gac tcg gaa gtt
738
Arg Ala Leu Glu Asn Pro Lys Ile Lys Val Leu Trp Asp Ser Glu Val
    205                      210                      215

gtc gag gcc tat ggc ggc gca aac ggc ggc cca ttg gct ggc gta aag
786
Val Glu Ala Tyr Gly Gly Ala Asn Gly Gly Pro Leu Ala Gly Val Lys
    220                      225                      230

gtt aag aac cta ctg aat ggt gag gtc tcg gat ctt cag gtg tct ggc
834
Val Lys Asn Leu Leu Asn Gly Glu Val Ser Asp Leu Gln Val Ser Gly
    235                      240                      245

ctc ttc ttc gcc atc ggg cat gag ccg gcg acc aaa ttc ctg ggc gga
882
Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly Gly
    250                      255                      260

cag ctt gaa ctc gat tca gat ggt tat gtg gaa acc aag cca ggt tcc
930
Gln Leu Glu Leu Asp Ser Asp Gly Tyr Val Glu Thr Lys Pro Gly Ser
265                      270                      275                      280

act cac acc agt gta aag ggt gta ttt gct gct ggc gac gtg cag gac
978
Thr His Thr Ser Val Lys Gly Val Phe Ala Ala Gly Asp Val Gln Asp
    285                      290                      295

aag aag tac cgt cag gcc att act gcc gct gga tca ggg tgc atg gct
1026
Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met Ala
    300                      305                      310

gca ttg gac gct gag cac tac ctg cag gag atc ggt gca cag gag gga
1074
Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Ile Gly Ala Gln Glu Gly
    315                      320                      325

aag tct gat tga ctatatttag gtgtagcaac cagcaatcca tcgaatagtc
1126

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241421.txt

Lys Ser Asp
330

agttgtcggg gctgaaagcc gctctctgat gcgcgtttat gccatgggtt gtcattgagct
1186

cacgattgag atacctgatg atttatgctg cttagtagca tgctattctt atcgtagga
1246

tccagaagta tgtctgaact ctgaactatt tactggatac ctattcgtga ttactgcctt
1306

gaagtttttc cttagatatc aaaaaaaaaa
1336

<210> 25
<211> 331
<212> PRT
<213> Zea mays

<400> 25

Met Glu Gly Ser Ala Ala Ala Pro Leu Arg Thr Arg Ile Cys Ile Ile
1 5 10 15

Gly Ser Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala
20 25 30

Glu Leu Lys Pro Val Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala
35 40 45

Ala Gly Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly
50 55 60

Phe Pro Asn Gly Ile Met Gly Ala Asp Leu Met Asp Asn Cys Arg Ala
65 70 75 80

Gln Ser Leu Arg Phe Gly Thr Asn Ile Leu Ser Glu Thr Val Thr Ala
85 90 95

Val Asp Phe Ser Ala Cys Pro Phe Arg Val Ser Ala Asp Ser Thr Thr
100 105 110

Val Leu Ala Asp Ala Val Ile Val Ala Thr Gly Ala Val Ala Arg Arg
115 120 125

Leu His Phe Pro Gly Ser Asp Ala Tyr Trp Asn Arg Gly Ile Ser Ala
130 135 140

TOE02T 624500T

241421.txt

Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys Pro Ile
145 150 155 160

Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ser Asn Phe Leu
165 170 175

Thr Lys Tyr Gly Ser His Val Tyr Ile Ile His Arg Arg Asn Thr Phe
180 185 190

Arg Ala Ser Lys Ile Met Gln Ala Arg Ala Leu Glu Asn Pro Lys Ile
195 200 205

Lys Val Leu Trp Asp Ser Glu Val Val Glu Ala Tyr Gly Gly Ala Asn
210 215 220

Gly Gly Pro Leu Ala Gly Val Lys Val Lys Asn Leu Leu Asn Gly Glu
225 230 235 240

Val Ser Asp Leu Gln Val Ser Gly Leu Phe Phe Ala Ile Gly His Glu
245 250 255

Pro Ala Thr Lys Phe Leu Gly Gly Gln Leu Glu Leu Asp Ser Asp Gly
260 265 270

Tyr Val Glu Thr Lys Pro Gly Ser Thr His Thr Ser Val Lys Gly Val
275 280 285

Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala Ile Thr
290 295 300

Ala Ala Gly Ser Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr Leu
305 310 315 320

Gln Glu Ile Gly Ala Gln Glu Gly Lys Ser Asp
325 330